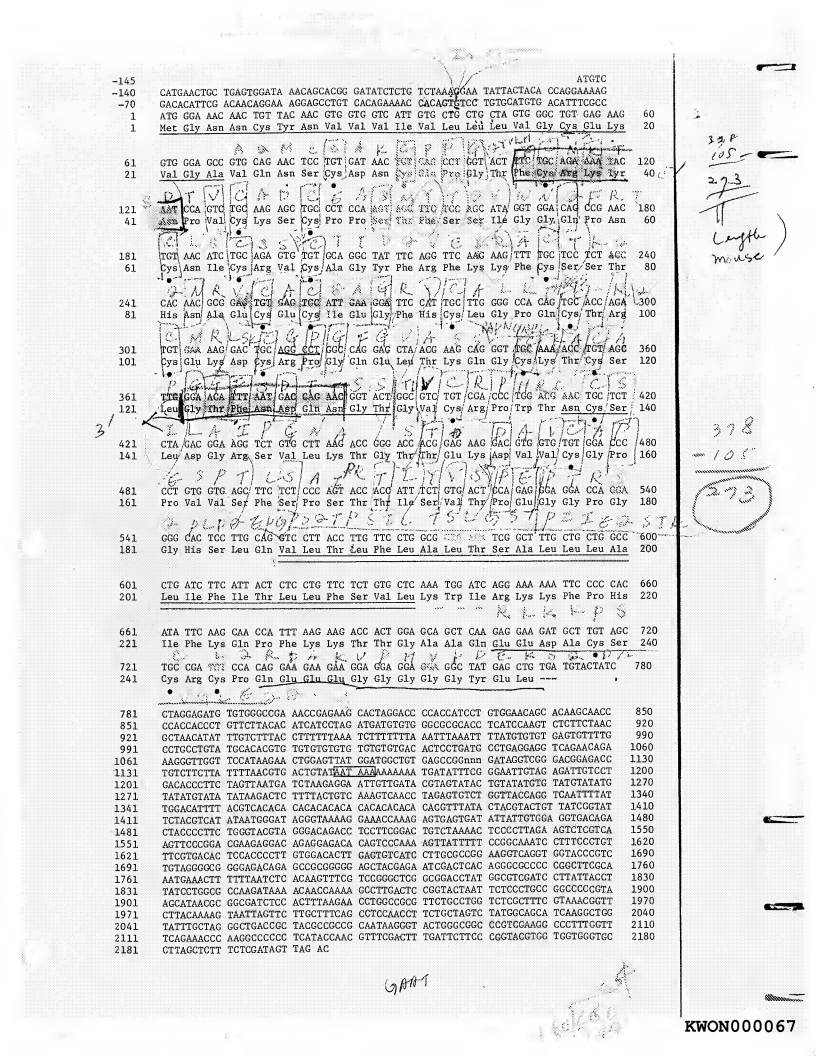
# EXHIBIT 9



-145 ATGTC
-140 CATGAACTGC TGAGTGGATA AACAGCACGG GATATCTCTG TCTAAAGCAA TATTACTACA CCAGGAAAAG
-70 GACACATTCG ACAACAGGAA AGGAGCCTGT CACAGAAAAC CACAGTGTCC TGTGCATGTG ACATTTCGCC
1 ATG GGA AAC AAC TGT TAC AAC GTG GTG GTC ATT GTG CTG CTG CTA GTG GGC TGT GAG AAG 60
1 Met Gly Asn Asn Cys Tyr Asn Val Val Val Ile Val Leu Leu Leu Val Gly Cys Glu Lys 20

61 GTG GGA GCC GTG CAG AAC TCC TGT GAT AAC TCC GAC CCT GGT ACT ATC TGC AGA AAA TAC 120
21 Val Gly Ala Val Gln Asn Ser Cys Asp Asn Ser Asp Pro Gly Thr Ile Cys Arg Lys Tyr 40

121 AAT CCA GTG TGC AAG AGC TGC CCT CCA AGT AGC TTC TCC AGC ATA GGT CGA CAG CCG AAC 180
41 Asn Pro Val Cys Lys Ser Cys Pro Pro Ser Thr Phe Ser Ser Ile Gly Gly Gln Pro Asn 60

181 TGT AAC ATC TGC AGA GTG TGT GCA GGC TAT TTC AGG TTC AAG AAG TTT TGC TCC TCT ACC 240
61 Cys Asn Ile Cys Arg Val Cys Ala Gly Tyr Phe Arg Phe Lys Lys Phe Cys Ser Ser Thr 80

241 CAC AAC GCG GAG TGT GAG TGC ATT GAA GGA TTC CAT TGC TTG GGG CCA CAG TGC ACC AGA 300
81 His Asn Ala Glu Cys Glu Cys Ile Glu Gly Phe His Cys Leu Gly Pro Gln Cys Thr Arg 100

301 TGT GAA AAG GAC TGC ACC CCT CCT CAG GAG CTA AGG AAC CAG GGT TCC AAA AGC TCT AGC 360
101 Cys Glu Lys Asp Cys Arg Pro Gly Gln Glu Leu Thr Lys Gln Gly Cys Lys Thr Cys Ser 120

361 TTT GCA ACA TTT AAT GAC GAC AAC GGT ACT GGC GTC TGT CGA CCC TGG ACG AAC TGC TCT 420
121 Leu Gly Thr Phe Asn Asp Asn Asn Gly Thr Gly Val Cys Arg Pro Trp Thr Asn Cys Ser 140

421 CTA GAC GGA AGG TCT GTG CTT AAG ACC GGG ACC ACG GAG AAG GAC GTG GTG TGT GGA CCC 480
141 Leu Asp Gly Arg Ser Val Leu Lys Thr Gly Thr Thr Glu Lys Asp Val Val Cys Gly Pro 160

481 CCT GTG GTG AGC TTC TCT CCC AGT ACC ACG ATT TCT CTG ACT CCA GAG GGA GCA CCA GGA 540
161 Pro Val Val Ser Phe Ser Pro Ser Thr Thr Ile Ser Val Thr Pro Glu Gly Gly Pro Gly 180

541 GGG CAC TCC TTG CAG GTC CTT ACC TTG TTC CTG GCG TCC TCG GCT TTG CTG CTG GCC 600
181 Gly His Ser Leu Gln Val Leu Thr Leu Phe Leu Ala Leu Thr Ser Ala Leu Leu Ala 200

601 CTG ATC TTC ATT ACT CTC CTG TTC TCT GTG CTC AAA TGG ATC AGG AAA AAA TTC CCC CAC 660
201 Leu Ile Phe Ile Thr Leu Leu Phe Ser Val Leu Lys Trp Ile Arg Lys Lys Phe Pro His 220

661 ATA TTC AAG CAA CCA TTT AAG AAG ACC ACT GGA GCA GCT CAA GAG GAA GAT GCT TGT AGC 720
221 Ile Phe Lys Gln Pro Phe Lys Lys Thr Thr Gly Ala Ala Gln Glu Glu Asp Ala Cys Ser 240

721 TGC CGA TGT CCA CAG GAA GAA GAA GGA GGA GGA GGA GGC TAT GAG CTG TGA TGTACTATC 780
241 Cys Arg Cys Pro Gln Glu Glu Glu Gly Gly Gly Gly Gly Tyr Glu Leu ---

781 CTAGGAGATG TGTGGGCCGA AACCGAGAAG CACTAGGACC CCACCATCCT GTGGAACAGC ACAAGCAACC 850
851 CCACCACCCT GTTCTTACAC ATCATCCTAG ATGATCTGTG GGCGCGCACC TCATCCAAGT CTCTTCTAAC 920
921 GCTAACATAT TTGTCTTTAC CTTTTTTAAA TCTTTTTTTA AATTTAAATT TTATGTGTGT GAGTGTTTTG 990
991 CCTGCCTGTA TGCACACGTG TGTGTGTGTG TGTGTGTGAC ACTCCTGATG CCTGAGGAGG TCAGAACAGA 1060
1061 AAGGGTTGGT TCCATAAGAA CTGGAGTTAT GGATGGCTGT GAGCCGGnnn GATAGGTCGG GACGGAGACC 1130
1131 TGTCTTCTTA TTTTAACGTG ACTGTATAAT AAAAAAAAAA TGATATTTCG GGAATTGTAG AGATTGTCGT 1200
1201 GACACCCTTC TAGTTAATGA CTAAAGAGGA ATTGTTGATA CGTAGTATAC TGTATATGTG TATCTATATC 1270
1271 TATATGTATA TATAGACTTC TTTTACTGTC AAAGTCAACC TAGAGTCGTC GCTTACCAGG TCAATTTTAT 1340
1341 TGGACATTTT ACGTCACACA CACACACACA CACACACACA CACGTTTATA CTAGGTACTG TATCGGTAT 1410
1411 TCTACGTCAT ATAATGGGAT AGGGTAAAAG GAAACCAAAG AGTGAGTGAT ATTATTGTGA GGTGACAGA 1480
1481 CTACCCCTTC TGGGTACGTA GGGACAGACC TCCTTCGGAC TGTCTAAAAC TCCCCTTAGA AGTCTCGTCA 1550
1551 AGTTCCCGGA CGAAGAGGAC AGAGGAGACA CAGTCCCAAA AGTTATTTTT CCGGCAAATC CTTTCCGTGT 1620
1621 TTCGTGACAC TCGACCCCTT GTGGACACTT GAGTGTCATC CTTGCGCCGC AAGGTCAGGT GGTACCGTCC 1690
1691 TGTAGGGGCG GGGAGACAGA GCCGCGGGGG AGCTACGAGA ATCGACTCAC AGGCGCCCC CGGCTTGCCA 1760
1761 AATGAAACTT TTTAATCTC ACAAGTTTCG TCCGGGCTGC GCGGACCTAT GGCGTCGATC CTTATTACCT 1830
1831 TATCCTGGCG CCAAGATAAA ACAACCAAAA GCCTTGACTC CGGTACTAAT TCTCCCTGCC GGCCCCGTA 1900
1901 AGCATAAGGC GGCGATCTCC ACTTTAAGAA CCTGGCCGCG TCTTCGCTTG CTCGCCTTTC GTAAACGGTT 1970
1971 CTTACAAAAG TAATTAGTTC TTGCTTTCAG CCTCCAACCT TCTGCTAGTC TATGGCAGCA TCAAGGCTGG 2040
2041 TATTTGCTAG GGCTGACCGC TACGCCGCCG CAATAAGGGT ACTGGCGGC CCGTCGAAGG CCCTTTGGTT 2110
2111 TCAGAAACCC AAGGCCCCCC TCATACCAAC GTTTCGACTT TGATTCTTCC CGGTAGGTGG TGGTGGGTGC 2180
2181 CTTAGCTCTT TCTCGATAGT TAG AC